

# SCORE Search Results Details for Application 10797393 and Search Result 20070118\_073132\_us-10-797-393a-1.rag.

Score Home Page Retrieve Application List SCORE System Overview SCORE\_FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10797393 and Search Result 20070118\_073132\_us-10-797-393a-1.rag.  
start | next page

Go Back to previous page

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: January 18, 2007, 09:03:27 ; Search time 197 Seconds  
(without alignments)  
1123.313 Million cell updates/sec  
Title: US-10-797-393A-1  
Perfect score: 2585  
Sequence: 1 LSASWRTQSIYPLLTDRFG.....PASVDSLLCGSGRLVYE 484

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2589679 seqs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:  
1: Geneseqp1980s:  
2: Geneseqp1990s:  
3: Geneseqp2000s:  
4: Geneseqp2001s:  
5: Geneseqp2002s:  
6: Geneseqp2003as:  
7: Geneseqp2003bs:  
8: Geneseqp2004s:  
9: Geneseqp2005s:  
10: Geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match Length	ID	Description
-----				

1	2585	100.0	484	5	AAE24207	Aae24207 Aspergill
2	2585	100.0	484	8	ADSV5939	Adsv5939 Aspergill
3	2585	100.0	484	9	ADSV5939	Adsv5939 Aspergill
4	2585	100.0	484	9	ADSV5939	Adsv5939 Aspergill
5	2585	100.0	484	9	ADSV5939	Adsv5939 Aspergill
6	2585	100.0	484	10	ADSV5939	Adsv5939 Aspergill
7	2544	98.4	476	9	ADSV5939	Adsv5939 Aspergill
8	2544	98.3	476	9	ADSV5939	Adsv5939 Aspergill
9	2537	98.1	476	9	ADSV5939	Adsv5939 Aspergill
10	2537	98.1	476	9	ADSV5939	Adsv5939 Aspergill
11	2537	98.1	476	9	ADSV5939	Adsv5939 Aspergill
12	2536	98.1	476	9	ADSV5939	Adsv5939 Aspergill
13	2536	98.1	476	9	ADSV5939	Adsv5939 Aspergill
14	2536	98.1	476	9	ADSV5939	Adsv5939 Aspergill
15	2503	96.8	505	9	ADSV5939	Adsv5939 Aspergill
16	2503	96.8	505	9	ADSV5939	Adsv5939 Aspergill
17	2501.5	96.8	505	9	ADSV5939	Adsv5939 Aspergill
18	2483	96.1	511	9	ADSV5939	Adsv5939 Aspergill
19	2483	96.1	588	9	ADSV5939	Adsv5939 Aspergill
20	2483	96.1	608	9	ADSV5939	Adsv5939 Aspergill
21	2483	96.1	609	9	ADSV5939	Adsv5939 Aspergill
22	2483	96.1	619	9	ADSV5939	Adsv5939 Aspergill
23	2483	96.1	629	9	ADSV5939	Adsv5939 Aspergill
24	2483	96.1	640	9	ADSV5939	Adsv5939 Aspergill
25	2436	94.2	480	10	ADSV5939	Adsv5939 Aspergill
26	2436	94.2	480	10	ADSV5939	Adsv5939 Aspergill
27	2436	94.2	619	10	ADSV5939	Adsv5939 Aspergill
28	2436	94.2	619	10	ADSV5939	Adsv5939 Aspergill
29	2436	94.2	640	10	ADSV5939	Adsv5939 Aspergill
30	2436	94.2	640	10	ADSV5939	Adsv5939 Aspergill
31	2427	93.9	640	9	ADSV5939	Adsv5939 Aspergill
32	2427	93.9	640	9	ADSV5939	Adsv5939 Aspergill
33	2427	93.9	640	9	ADSV5939	Adsv5939 Aspergill
34	2420	93.6	619	9	ADSV5939	Adsv5939 Aspergill
35	2420	93.6	619	9	ADSV5939	Adsv5939 Aspergill
36	1940.5	75.1	630	6	ADSV5939	Adsv5939 Aspergill
37	1846	71.4	608	9	ADSV5939	Adsv5939 Aspergill
38	1842	71.3	608	9	ADSV5939	Adsv5939 Aspergill
39	1839	71.1	608	9	ADSV5939	Adsv5939 Aspergill
40	1834	70.9	608	9	ADSV5939	Adsv5939 Aspergill
41	1830	70.8	608	9	ADSV5939	Adsv5939 Aspergill
42	1826	70.6	608	9	ADSV5939	Adsv5939 Aspergill
43	1821	70.4	608	9	ADSV5939	Adsv5939 Aspergill
44	1818	70.3	608	9	ADSV5939	Adsv5939 Aspergill
45	1817	70.3	608	9	ADSV5939	Adsv5939 Aspergill

## ALIGNMENTS

RESULT 1	
AAE24207	
ID	AAE24207 standard; protein; 484 AA.
AC	AAE24207;
XX	
DT	04-OCT-2002 (first entry)
XX	
DE	Aspergillus niger alpha-amylase protein.
XX	
KW	Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
XX	
OS	fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
XX	



Query Match	100.0%; Score 2585; DB 8; Length 484;
Best Local Similarity	100.0%; Pred. No. 3.9e-198;
Matches 484; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LSAASRQTOSYIFLLTDRFGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60
DB	1 LSAASRQTOSYIFLLTDRFGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60
QY	61 WISPIEQLPQDTADGEAYHGVWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVP 120
DB	61 WISPIEQLPQDTADGEAYHGVWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVP 120
QY	121 DHMGYAGNGNDVSVDFPSSSYFHPYCLITDNDLTMVEDCWEGDTIVSLPDLDTTE 180
DB	121 DHMGYAGNGNDVSVDFPSSSYFHPYCLITDNDLTMVEDCWEGDTIVSLPDLDTTE 180
QY	181 TAVRTIYDWADLVSNYSVDGLRIDSLEVPDFFPGYNKASGVYCVGEIDNGNPASDC 240
DB	181 TAVRTIYDWADLVSNYSVDGLRIDSLEVPDFFPGYNKASGVYCVGEIDNGNPASDC 240
QY	241 PYQKVLGVLNYPYIYQWLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHNP 300
DB	241 PYQKVLGVLNYPYIYQWLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHNP 300
QY	301 FAKYTSQAKNVLSYIFLSDGIPYVAGEEQHYAGGVYVYVREATWLSGVDTSALYT 360
DB	301 FAKYTSQAKNVLSYIFLSDGIPYVAGEEQHYAGGVYVYVREATWLSGVDTSALYT 360
QY	421 LTLSSGYTSGTKLIEAYTCTSVTVSSGDIIPVPMASGLPRVLLPASVVDSSSLCGSGR 480
DB	421 LTLSSGYTSGTKLIEAYTCTSVTVSSGDIIPVPMASGLPRVLLPASVVDSSSLCGSGR 480
QY	481 LYVE 484
DB	481 LYVE 484
RESULT 3	
ADV09273	
ID	ADV09273 standard; protein; 484 AA.
XX	
AC	ADV09273;
XX	
DT	24-FEB-2005 (first entry)
XX	
DE	Aspergillus niger acid alpha-amyase amino acid sequence - SEQ ID 1.
XX	
KW	alcohol production ; starch hydrolysis; fuel ethanol; potable ethanol;
XX	
OS	industrial ethanol; enzyme; acid alpha-amyase.
XX	
XX	Aspergillus niger.
XX	
PN	W02004.106533-A1.
XX	
PD	09-DEC-2004.
XX	
PF	28-MAY-2004; 2004WO-DK000373.
XX	
PR	30-MAY-2003; 2003DK-00000812.
XX	
PA	(NOVO ) NOVOZYMES AS.

XX	Olsen HS, Norman BE, Wuempelmann M, Tams JW;
PI	WPI; 2005-021301/02.
XX	
DR	Producing an alcohol product, e.g. ethanol, comprises holding slurry at
XX	elevated temperature below the initial gelatinization temperature of the
PT	granular starch followed by saccharification and fermentation.
XX	
PS	Claim 9; SEQ ID NO 1; 43pp; English.
XX	
CC	The invention comprises a method for producing an alcohol product. The
XX	method involves holding a slurry of water and granular starch below the
CC	initial gelatinization temperature of the granular starch, and fermenting
XX	the slurry with a yeast to produce ethanol (where both steps are
CC	performed in the presence of an acid alpha-amyase, a maltose generating
XX	enzyme and an alpha-glucosidase). The method of the invention is useful
CC	in the hydrolysis of granular starch or a starch hydrolysis process. The
XX	method of the invention is useful for producing an alcohol product (e.g.
CC	fuel ethanol, potable ethanol and/or industrial ethanol). The present
XX	invention represents an Aspergillus niger alpha-amyase of the
CC	invention.
XX	
SEQ	Sequence 484 AA:
Query Match	100.0%; Score 2585; DB 9; Length 484;
Best Local Similarity	100.0%; Pred. No. 3.9e-198;
Matches 484; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LSAASRQTOSYIFLLTDRFGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60
DB	1 LSAASRQTOSYIFLLTDRFGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60
QY	61 WISPIEQLPQDTADGEAYHGVWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVP 120
DB	61 WISPIEQLPQDTADGEAYHGVWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVP 120
QY	121 DHMGYAGNGNDVSVDFPSSSYFHPYCLITDNDLTMVEDCWEGDTIVSLPDLDTTE 180
DB	121 DHMGYAGNGNDVSVDFPSSSYFHPYCLITDNDLTMVEDCWEGDTIVSLPDLDTTE 180
QY	181 TAVRTIYDWADLVSNYSVDGLRIDSLEVPDFFPGYNKASGVYCVGEIDNGNPASDC 240
DB	181 TAVRTIYDWADLVSNYSVDGLRIDSLEVPDFFPGYNKASGVYCVGEIDNGNPASDC 240
QY	241 PYQKVLGVLNYPYIYQWLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHNP 300
DB	241 PYQKVLGVLNYPYIYQWLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHNP 300
QY	301 FAKYTSQAKNVLSYIFLSDGIPYVAGEEQHYAGGVYVYVREATWLSGVDTSALYT 360
DB	301 FAKYTSQAKNVLSYIFLSDGIPYVAGEEQHYAGGVYVYVREATWLSGVDTSALYT 360
QY	361 WIATTNAIRKLAIAADSAYITVANDAFYTDNTIAMAKGTSGSQVITVLSNKGSGSSYT 420
DB	361 WIATTNAIRKLAIAADSAYITVANDAFYTDNTIAMAKGTSGSQVITVLSNKGSGSSYT 420
QY	421 LTLSSGYTSGTKLIEAYTCTSVTVSSGDIIPVPMASGLPRVLLPASVVDSSSLCGSGR 480
DB	421 LTLSSGYTSGTKLIEAYTCTSVTVSSGDIIPVPMASGLPRVLLPASVVDSSSLCGSGR 480
QY	481 LYVE 484
DB	481 LYVE 484

RESULT 4  
AEB72807  
ID AEB72807 standard; protein; 484 AA.  
XX AC AEB72807;  
XX DT 06-OCT-2005 (first entry)  
XX DE Fungal acid alpha-amylase.  
XX KW glucoamylase; fermentation; cereals; alcohol; ethanol; fuel ethanol;  
XX KW potable ethanol; industrial ethanol; gelatinization.  
XX OS Aspergillus niger.  
XX PN WO2005069840-A2.  
XX PD 04-AUG-2005.  
XX PF 14-JAN-2005; 2005WO-US0901147.  
XX PR 16-JAN-2004; 2004US-0537071P.  
XX PR 14-DEC-2004; 2004US-0636013P.  
XX PA (NOVO) NOVOZYMES NORTH AMERICA INC.  
XX PA (NOVO) NOVOZYMES AS.  
XX PI Allain E, Wenger KS, Bisgard-Frantzen H;  
XX WPI: 2005-542205/55.  
XX  
XX Producing fermentation product e.g. ethanol from starch-containing  
PT material involves saccharifying the material with specific glucoamylase,  
PT at temperature below initial gelatinization temperature of the material  
PT and fermenting.  
XX  
XX Disclosure; SEQ ID NO 3; 96pp; English.  
XX  
XX This sequence represents an acid alpha-amylase which was used in the  
CC method of the invention. The method for producing a fermentation product  
CC from milled starch-containing material involves: saccharifying milled  
CC starch-containing material with the glucoamylase from the fungi *Athelia*  
CC *rolfsii*, at temperature below the initial gelatinization temperature of  
CC starch containing material; and fermenting using a fermenting medium. The  
CC process is carried out for 1 - 250, especially 80 - 130 hours, at pH of 3  
CC - 7, especially 4 - 5. The dry solid (DS) content in the process is 20 -  
CC 55 (preferably 25 - 40, especially 30 - 35) wt.%. The sugar concentration  
CC is kept below 3 wt.% during saccharification and fermentation. A slurry  
CC of water and milled starch-containing material is prepared before step  
CC (a). The milled starch-containing material is prepared by milling starch-  
CC containing material to a particle size of 0.1 - 0.5 mm. The  
CC saccharification is carried out simultaneously. The fermentation is  
CC carried out at 28 - 36, especially 32 deg C. The glucoamylase is present  
CC in an amount of 0.01 - 10, especially 0.1 - 0.5 AGU/g DS. The  
CC fermentation product is recovered after fermentation. The process is  
CC carried out in the presence of a protease (preferably acid protease,  
CC especially fungal acid protease). The starch-containing material is  
CC obtained from tubers, roots, stems, seeds or whole grains of corn, cobs,  
CC wheat, barley, rye, milo, sago, cassava, manioc, tapioca, sorghum, rice  
CC or potatoes (preferably cereals). The method of the invention is for  
CC producing a fermentation product e.g. alcohol such as ethanol selected  
CC from fuel ethanol, potable ethanol and industrial ethanol. The method  
CC produces fermentation product without gelatinization of the starch-  
CC containing material; and produces ethanol in higher yield.

XX SQ Sequence 484 AA;  
Query Match 100.0%; Score 2585; DB 9; Length 484;  
Best Local Similarity 100.0%; Pred. No. 3.9e-198;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LSASWRTQSIYFLTDRFGTDMSTTATCTGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60  
DB 1 LSASWRTQSIYFLTDRFGTDMSTTATCTGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60  
QY 61 WISPITEQLPQDTADGEAYHGYYWQKIYDVNSNFTADNLKSLSDALHARGMYLWVDVP 120  
DB 61 WISPITEQLPQDTADGEAYHGYYWQKIYDVNSNFTADNLKSLSDALHARGMYLWVDVP 120  
QY 121 DHMGYAGNGNDVSVFPDSSSYFHPYCLITDNDLTMVEDCWECDTIVSLPDLDTTE 180  
DB 121 DHMGYAGNGNDVSVFPDSSSYFHPYCLITDNDLTMVEDCWECDTIVSLPDLDTTE 180  
QY 181 TAVRTIWDYVADLVSNYSVDGLRIDSLEVPDPFPGYNKASGVYCVGEIDNGNPASDC 240  
DB 181 TAVRTIWDYVADLVSNYSVDGLRIDSLEVPDPFPGYNKASGVYCVGEIDNGNPASDC 240  
QY 241 PYOKVLGVLNYPYIYQWLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHNP 300  
DB 241 PYOKVLGVLNYPYIYQWLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHNP 300  
QY 301 PAKYTSQAKNVLSYIFLSDGPIVYAGEEQHYAGKVPYNREATMLSGYDTSAELYT 360  
DB 301 PAKYTSQAKNVLSYIFLSDGPIVYAGEEQHYAGKVPYNREATMLSGYDTSAELYT 360  
QY 361 WIATNTRKLAIAADSAYITYANDAFYDTSNTTAMAKTSGSQVITVLSNKGSGSSYT 420  
DB 361 WIATNTRKLAIAADSAYITYANDAFYDTSNTTAMAKTSGSQVITVLSNKGSGSSYT 420  
QY 421 LTSGSGYTSGLKLEIAYTCTSVTVDSGDIPVPMASGLPRVLLPASVWVDSLSLCCGSGR 480  
DB 421 LTSGSGYTSGLKLEIAYTCTSVTVDSGDIPVPMASGLPRVLLPASVWVDSLSLCCGSGR 480  
QY 481 LYVE 484  
DB 481 LYVE 484  
RESULT 5  
AEC92136  
ID AEC92136 standard; protein; 484 AA.  
XX AC AEC92136;  
XX DT 01-DEC-2005 (first entry)  
XX DE Protein sequence of alpha amylase B.  
XX KW alpha-amylase B; fermentation; cereal; ethanol; sugar; oligosaccharide.  
XX OS Aspergillus niger.  
XX PN WO2005092015-A2.  
XX PD 06-OCT-2005.  
XX PF 18-MAR-2005; 2005WO-US009218.  
XX PR 19-MAR-2004; 2004US-0554615P.

PR 28-MAY-2004; 2004US-0575133P.  
XX (NOVO ) NOVOZYMES NORTH AMERICA INC.  
PA (NOVO ) NOVOZYMES AS.  
XX  
XX Bhargava S, Bisgard-Frantzen H, Frisner H, Vikso-Nielsen A;  
PI Jøhal W;  
XX WPI; 2005-676933/69.  
XX  
XX Liquefying starch-containing material by treating the starch-containing  
PT material with a bacterial alpha-amylase at set temperatures and for a  
PT defined period of time.  
XX  
XX Claim 15; SEQ ID NO 1; 30pp; English.  
XX  
XX The new invention relates to a method of liquefying starch-containing  
CC material by treating the material with a bacterial alpha-amylase at a  
CC temperature around 70-90 degrees C for 15-90 minutes; and treating the  
CC material with an alpha-amylase at a temperature between 60-80 degrees C  
CC for 30-90 minutes. Also claimed are a process of producing a fermentation  
CC product from starch-containing material by fermentation; and a process of  
CC producing syrup from starch-containing material. The starch-containing  
CC material comprises tubers, roots and/or whole grain, obtained from  
CC cereals such as corn, cob, wheat, barley, rye, milo and/or potatoes. The  
CC bacterial alpha-amylase is derived from *Bacillus stearothermophilus* alpha  
CC -amylase or a variant with the mutations: I181+G182 especially  
CC I181+G182+N193F. The alpha-amylase is an acid alpha-amylase, preferably  
CC an acid fungal alpha-amylase, preferably derived from *Aspergillus niger*  
CC or *Aspergillus oryzae*. The acid alpha-amylase is SEQ ID NO: 1. The method  
CC further comprises recovering the fermentation product, which is ethanol.  
CC The methods are useful for producing syrup from starch-containing  
CC material. The syrup is glucose, maltose, fructose syrups, malto-  
CC oligosaccharides or isomalto-oligosaccharides. The method is useful in  
CC liquefying starch-containing material for producing a fermentation  
CC product, preferably ethanol, or syrup, preferably glucose, maltose,  
CC fructose syrups, malto-oligosaccharides or isomalto-oligosaccharides. The  
CC preent sequence is the protein sequence of alpha amylase B.  
XX  
SQ Sequence 484 AA;

Query Match 100.0%; Score 2585; DB 9; Length 484;  
Best Local Similarity 100.0%; Pred. No. 3.9e-198;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSAASRQTQSYFLLDTRFGRDNTSTTATCTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60  
DB 1 LSAASRQTQSYFLLDTRFGRDNTSTTATCTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60  
QY 61 WISPIEQLPDTADCEAYHGYWQKIYDVNSNFTADNLKSLSDALHARGMYLWDVVP 120  
DB 61 WISPIEQLPDTADCEAYHGYWQKIYDVNSNFTADNLKSLSDALHARGMYLWDVVP 120  
QY 121 DHMGYAGNNDVYSVDFPDSSSYFHPYCLITDWNLTWEDCWECDTIVSLPDLDTTE 180  
DB 121 DHMGYAGNNDVYSVDFPDSSSYFHPYCLITDWNLTWEDCWECDTIVSLPDLDTTE 180  
QY 181 TAVRTTWDMVADLVSNYSVDGLRIDSVLEVPFPFGYNKASGVYCVGEIDNGNPSDC 240  
DB 181 TAVRTTWDMVADLVSNYSVDGLRIDSVLEVPFPFGYNKASGVYCVGEIDNGNPSDC 240  
QY 241 PYKRLDGLVLPYIYQQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHNPR 300  
DB 241 PYKRLDGLVLPYIYQQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHNPR 300

QY 301 FAKYTSVDSQAKNVLSTPLSDGPIPIVYAGEQHYAGGKVPYNREATMLSGYDTSAELYT 360  
DB 301 FAKYTSVDSQAKNVLSTPLSDGPIPIVYAGEQHYAGGKVPYNREATMLSGYDTSAELYT 360  
QY 361 WIATTNARKLATAADSAVITYYANDAPYTDSTNTANAKTSGSOVITVLNKGSGSSYT 420  
DB 361 WIATTNARKLATAADSAVITYYANDAPYTDSTNTANAKTSGSOVITVLNKGSGSSYT 420  
QY 421 LTLSSGYTSGTKLIEAYTCTSVTVDSSGDIPIVPMASGLPRVLLPASVWVSSSLCGGSGR 480  
DB 421 LTLSSGYTSGTKLIEAYTCTSVTVDSSGDIPIVPMASGLPRVLLPASVWVSSSLCGGSGR 480  
QY 481 LYWE 484  
DB 481 LYWE 484  
RESULT 6  
AEE27539  
ID AEE27539 standard; protein; 484 AA.  
XX  
AC AEE27539;  
XX  
DT 09-FEB-2006 (first entry)  
XX  
DE Fungal acid alpha-amylase B protein sequence.  
XX  
KW fermentation; ethanol; fuel; acid alpha-amylase;  
KW 1.4-alpha-D-glucan glucanohydrolase; enzyme; E.C.3.2.1.1.  
OS *Aspergillus niger*.  
XX  
PN W02005113785-A2.  
XX  
PD 01-DEC-2005.  
XX  
PF 11-MAY-2005; 2005WO-US016390.  
PR 13-MAY-2004; 2004US-0570727P.  
PR 01-DEC-2004; 2004US-0632201P.  
PR 03-DEC-2004; 2004US-0632293P.  
XX  
PA (NOVO ) NOVOZYMES NORTH AMERICA INC.  
PA (NOVO ) NOVOZYMES AS.  
XX  
PI Bhargava S, Frisner H, Bisgard-Frantzen H, Tang JW;  
XX  
XX WPI; 2006-010609/01.  
DR SWISSPROT; P56271.  
XX  
XX Producing a fermentation product (preferably ethanol) from a starch-  
PT containing material, comprises treatment with alpha-amylase, and then  
PT alpha-glucosidase, before fermentation with a fermenting organism.  
XX  
XX Claim 11; SEQ ID NO 1; 54pp; English.  
XX  
XX The new invention relates to a method of producing (M1) a fermentation  
CC product from starch-containing materials. The method comprises subjecting  
CC starch-containing material to an alpha-amylase, subjecting the obtained  
CC material to an alpha-glucosidase and optionally a glucose-generating  
CC and/or maltose-generating enzyme, and fermenting the material in the  
CC presence of a fermenting organism. In (M1), the fermentation product is  
CC recovered after fermentation, preferably by distillation. (M1) is useful  
CC for producing a fermentation product from starch-containing materials,  
CC where the fermentation product is ethanol, which is useful as e.g. fuel

CC ethanol, drinking ethanol (such as potable neutral spirits), or  
CC industrial ethanol, including fuel additive. The present sequence is a  
CC fungal acid alpha amylase B (FAAB). (1.4-alpha-D-glucan  
XX glucanohydrolase).

XX Sequence 484 AA;

Query Match 100.0%; Score 2585; DB 10; Length 484;  
Best Local Similarity 100.0%; Pred. No. 3.9e-198;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSAASWRTQSIYFLITDRPGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60  
DB 1 LSAASWRTQSIYFLITDRPGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60  
QY 61 WISPIITEQLPQDTADGEAYHGYWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVVP 120  
DB 61 WISPIITEQLPQDTADGEAYHGYWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVVP 120  
QY 121 DHMGYAGNNDVYSVPDFDSSSYFHPYCLITDNDLNTWVEDCWEGDTIVSLPDLDTTE 180  
DB 121 DHMGYAGNNDVYSVPDFDSSSYFHPYCLITDNDLNTWVEDCWEGDTIVSLPDLDTTE 180  
QY 181 TAVRTTWDMVADLVSNYSVDGLRIDSVLEVPDPFGYNKASGVYCVGEIDNGNPASDC 240  
DB 181 TAVRTTWDMVADLVSNYSVDGLRIDSVLEVPDPFGYNKASGVYCVGEIDNGNPASDC 240  
QY 241 PYQKVLGVLNYPYIYQWLLYAFESSGSIINLYMKSVASDCSDPTLLGNFIENHNP 300  
DB 241 PYQKVLGVLNYPYIYQWLLYAFESSGSIINLYMKSVASDCSDPTLLGNFIENHNP 300  
QY 301 FAKYTSQKQNVLSYIFLSDGPIVYAGEEYHAGGVYVREATWLSGYDTSALYV 360  
DB 301 FAKYTSQKQNVLSYIFLSDGPIVYAGEEYHAGGVYVREATWLSGYDTSALYV 360  
QY 361 WIATTNARKLAIAADSAVITYANDAFYTDSTNTANAKGTSGSQVITVLSNKGSGSSYT 420  
DB 361 WIATTNARKLAIAADSAVITYANDAFYTDSTNTANAKGTSGSQVITVLSNKGSGSSYT 420  
QY 421 LTLSSGVTSGTKLIEAYTCTSVTVDSGDIYVPMASGLPRVLLPASVVDSSSLCGSGR 480  
DB 421 LTLSSGVTSGTKLIEAYTCTSVTVDSGDIYVPMASGLPRVLLPASVVDSSSLCGSGR 480  
QY 481 LYVE 484  
DB 481 LYVE 484

#### RESULT 7

ID ADY52195  
AC ADY52195 standard; protein; 476 AA.

XX ADY52195;

XX 19-MAY-2005 (first entry)

XX Aspergillus niger alpha-amylase.

XX alpha amylase; hydrolysis; starch; bread; anti-staling; enzyme.

XX Aspergillus niger.

XX W02005019443-A2.

XX 03-MAR-2005.

XX 23-AUG-2004; 2004WO-DK000558.  
XX 22-AUG-2003; 2003DK-00001201.  
XX (NOVO) NOVOZYMES AS.

XX Svendsen A, Beier L, Vind J, Spendler T, Jensen MT;

XX WPI; 2005-202646/21.

XX Producing fungal alpha-amylase variants which is useful for preparing  
XX dough or baked from dough product, based on comparison of three-  
XX dimensional structures of fungal alpha-amylase and maltogenic alpha-  
XX amylase.

XX Claim 11; SEQ ID NO 3; 26pp; English.

XX The invention relates to a method of producing a variant fungal alpha-  
XX amylase by superimposing a three-dimensional (3D) model for a fungal  
XX alpha-amylase and a 3D model for a maltogenic alpha-amylase, selecting an  
XX amino acid residue in the fungal amylase which has a C-alpha atom located  
XX greater than 0.8 Angstrom from the C-alpha atom of amino acid residue in  
XX the maltogenic alpha-amylase and less than 11 Angstrom from an atom of an  
XX enzyme substrate, altering the fungal amylase sequence, and producing the  
XX variant polypeptide. Also described are (i) a polypeptide comprising (a)  
XX an amino acid sequence having at least 70% identity to a fully defined  
XX 476 amino acids (SEQ ID No:2) sequence given in the specification, and  
XX compared to SEQ ID No:2 comprises an amino acid alteration which is a  
XX deletion, substitution or insertion at a position corresponding to 15, 32  
XX -36, 63-64, 73-77, 119-120, 125-126, 151-152, 155-156, 167-172, 211 or  
XX 233-239, and has the ability to hydrolyze starch, (b) has an amino acid  
XX sequence having at least 70% identity to a fully defined 476 amino acids  
XX (SEQ ID No:3) sequence given in the specification, compared to SEQ ID  
XX No:3 comprises an amino acid alteration which comprises Q35K, Q35R, P70K,  
XX L151P, L151D, N233G-G234D, D75G, D75A or 166-171 (Glu-Gly-Asp-Thr-Ile-  
XX Val) substituted with Phe-Thr-Asp-Pro-Ala-Gly-Phe, and has the ability to  
XX hydrolyze starch, or (c) has an amino acid sequence having at least 70%  
XX identity to a fully defined 476 amino acids (SEQ ID No:4) sequence given  
XX in the specification, compared to SEQ ID No:4 comprises an amino acid  
XX alteration which comprises G35K, G35R, A76deletion-D77deletion,  
XX D74deletion-A78deletion, D74A, D74G, D77A, D77G, Y157W or  
XX L168F-A169T-T171P-P172A-T173G, and has the ability to hydrolyze starch.  
XX The method of the invention is useful for producing a variant fungal  
XX alpha-amylase. The polypeptide produced by the method is useful for  
XX preparing a dough, or a product baked from dough. The polypeptide of the  
XX method is useful for anti-staling in baked products. The variant  
XX polypeptide has improved anti-staling effect and a higher degree of exo-  
XX amylase activity. This sequence represents Aspergillus niger alpha-  
XX amylase.

XX Sequence 476 AA;

Query Match 98.4%; Score 2544; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7.4e-195;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSAASWRTQSIYFLITDRPGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60  
DB 1 LSAASWRTQSIYFLITDRPGRTDNSTTATCTNGNEIYCGSGWQGIIDHLDYIEGNGFTAI 60  
QY 61 WISPIITEQLPQDTADGEAYHGYWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVVP 120  
DB 61 WISPIITEQLPQDTADGEAYHGYWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVDVVP 120

# SCORE Search Results Details for Application 10797393 and Search Result 20070118\_073134\_us-10-797-393a-1.rup.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10797393 and Search Result 20070118\_073134\_us-10-797-393a-1.rup.  
start | next page

Go Back to previous page

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: January 18, 2007, 09:04:22 : Search time 303 Seconds  
(without alignments)  
1477.583 Million cell updates/sec  
Title: US-10-797-393A-1  
Perfect score: 2585  
Sequence: 1 LSNASWRTQSIYFLLTDRFG.....PASVVDSSILCGSGRLVYE 484  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2849598 seqs, 945015592 residues  
Total number of hits satisfying chosen parameters: 2849598  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0t  
Maximum Match 100t  
Listing first 45 summaries  
Database : Uniprot\_7.2:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2585	100.0	484	1 AMYA ASPNG	P56271 aspergillus
2	2427	93.9	640	2 Q13296 ASPKA	Q13296 aspergillus
3	2390.5	92.5	634	2 Q76196 ASPAW	Q76196 aspergillus
4	1940.5	75.1	630	2 Q4WIT5 ASPFU	Q4WIT5 aspergillus
5	1780	68.9	499	2 Q7LV45 ASPPL	Q7LV45 aspergillus
6	1780	68.9	499	2 Q96TH4 ASPOR	Q96TH4 aspergillus
7	1778	68.8	498	2 Q76CT3 ASPKA	Q76CT3 aspergillus
8	1778	68.8	499	1 AMYA ASPOR	P10529 aspergillus

## SUMMARIES

9	1778	68.8	499	2	Q2U6K7 ASPOR	Q2U6K7 aspergillus
10	1774	68.6	499	2	Q76L99 ASPAW	Q76L99 aspergillus
11	1772	68.5	499	1	AMYE ASPAW	Q02906 aspergillus
12	1771	68.5	498	1	AMYA ASPAW	Q02905 aspergillus
13	1769	68.4	499	1	AMY ASPH	P10292 aspergillus
14	1701.5	65.8	494	2	Q4WPQ3 ASPFU	Q4WPQ3 aspergillus
15	1670	64.6	623	2	Q9UUV9 EMENI	Q9UUV9 emericella
16	1670	64.6	623	2	Q5B7S8 EMENI	Q5B7S8 aspergillus
17	1578	61.0	490	2	Q9UUV7 EMENI	Q9UUV7 emericella
18	1578	61.0	490	2	Q5B8R2 EMENI	Q5B8R2 aspergillus
19	1453	56.2	647	2	Q6VF33 LIPST	Q6VF33 lipomyces s
20	1425	55.1	624	1	AMY1 LIPKO	Q01117 lipomyces k
21	1387	53.7	507	1	AMY2 DEBOC	Q08806 debaryomyce
22	1304.5	50.5	512	1	AMY1 DEBOC	P19269 debaryomyce
23	1291.5	50.0	494	1	AMY1 SACFI	P21567 saccharomyc
24	1247	48.2	631	2	Q92394 9HETE	Q92394 cryptococcu
25	1151	44.5	561	2	Q4X0H4 ASPFU	Q4X0H4 aspergillus
26	1146	44.3	549	2	Q2UISS ASPOR	Q2UISS aspergillus
27	1131.5	43.8	492	2	Q7SDJ6 NEURC	Q7SDJ6 neurospora
28	1115.5	43.2	568	2	Q4W135 ASPFU	Q4W135 aspergillus
29	1098.5	42.5	521	2	Q5B4M3 EMENI	Q5B4M3 aspergillus
30	1090.5	42.2	559	2	Q5AZF6 EMENI	Q5AZF6 aspergillus
31	1088	42.1	552	2	Q5B822 EMENI	Q5B822 aspergillus
32	1062	41.1	561	2	Q4W4V4 ASPFU	Q4W4V4 aspergillus
33	1061.5	41.1	532	2	Q2KHCO MAGGR	Q2KHCO magnaporthe
34	1057	40.9	532	2	Q5SS33 CRINE	Q5SS33 cryptococcu
35	1057	40.9	532	2	Q5KGI6 CRINE	Q5KGI6 cryptococcu
36	1001	38.7	533	2	Q7S4K0 NEURC	Q7S4K0 neurospora
37	908	35.1	513	1	AMY3 SCHPO	Q14154 schizosacch
38	903.5	35.0	572	2	Q5K9B2 CRINE	Q5K9B2 cryptococcu
39	902.5	34.9	572	2	Q5K993 CRINE	Q5K993 cryptococcu
40	901	34.9	625	2	Q74922 SCHPO	Q74922 schizosacch
41	852.5	33.0	564	1	AMY4 SCHPO	Q9Y789 schizosacch
42	845	32.7	460	2	Q4IG16 GIBZE	Q4IG16 gibberella
43	837.5	32.4	561	2	Q5KPY6 CRINE	Q5KPY6 cryptococcu
44	835.5	32.3	600	2	Q2KEQ7 MAGGR	Q2KEQ7 magnaporthe
45	832	32.2	460	2	Q3YBZ7 GIBMO	Q3YBZ7 gibberella

## ALIGNMENTS

RESULT 1	ID	AMYA ASPNG	STANDARD	PRT	484 AA
AC	P56271				
DT	15-JUL-1998	Integrated into UniProtKB/Swiss-Prot.			
DT	15-JUL-1998	sequence version 1.			
DT	07-FEB-2006	entry version 34.			
DE	Acid alpha-amyase (EC 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase).				
OS	Aspergillus niger.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.				
OX	NCBI_TaxID=5061;				
RN	[1]				
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).				
RX	MEDLINE=91002514; Pubmed=2207069;				
RA	Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,				
RA	Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.P.;				
RT	*Calcium binding in alpha-amyases: an X-ray diffraction study at 2.1-				
RT	A resolution of two enzymes from Aspergillus.*;				
RL	Biochemistry 29:6244-6249(1990).				
CC	- - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-D-glucosidic				
CC	linkages in oligosaccharides and polysaccharides.				
CC	- - COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory				

CC at high concentrations.  
CC -!- SUBUNIT: Monomer.  
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC -----  
DR PDB; 2AAA; X-ray; 0=1-484.  
DR LinkHub; P56271; -  
DR InterPro; IPR006589; Alp\_amy1\_cat sub.  
DR InterPro; IPR006047; Alpha\_amy1\_cat.  
DR Pfam; PF00128; Alpha-amyase; 1.  
DR SMART; SM00642; Amy; 1.  
KW 3D-structure; Calcium; Carbohydrate metabolism; Glycoprotein;  
KW Glycosidase; Hydrolase; Metal-binding.  
FT CHAIN 1 484  
FT FT 206 206  
FT ACT\_SITE 230 230  
FT ACT\_SITE 297 297  
FT METAL 121 121  
FT METAL 162 162  
FT METAL 175 175  
FT METAL 206 206  
FT METAL 210 210  
FT METAL 230 230  
FT CARBOHYD 24 24  
FT CARBOHYD 157 157  
FT CARBOHYD 197 197  
FT DISULFID 30 38  
FT DISULFID 150 164  
FT DISULFID 240 283  
FT DISULFID 440 475  
FT HELIX 3 6  
FT TURN 7 8  
FT STRAND 11 13  
FT HELIX 16 19  
FT TURN 22 23  
FT STRAND 26 26  
FT HELIX 32 34  
FT STRAND 36 36  
FT HELIX 42 47  
FT TURN 48 48  
FT HELIX 49 53  
FT TURN 54 56  
FT STRAND 59 62  
FT STRAND 66 68  
FT STRAND 73 73  
FT TURN 74 75  
FT STRAND 76 76  
FT STRAND 78 78  
FT TURN 79 80  
FT STRAND 81 81  
FT STRAND 83 90  
FT TURN 92 94  
FT HELIX 97 108  
FT TURN 109 111  
FT STRAND 113 118  
FT STRAND 121 122  
FT STRAND 125 127  
FT HELIX 129 131  
FT HELIX 134 136  
FT STRAND 137 139  
FT STRAND 142 142  
FT HELIX 143 145

FT STRAND 146 146  
FT STRAND 151 151  
FT TURN 155 156  
FT HELIX 158 163  
FT STRAND 164 167  
FT STRAND 169 173  
FT STRAND 175 176  
FT TURN 178 179  
FT STRAND 180 180  
FT HELIX 181 198  
FT TURN 199 199  
FT STRAND 202 206  
FT STRAND 208 208  
FT TURN 209 210  
FT STRAND 211 211  
FT HELIX 213 223  
FT TURN 224 224  
FT STRAND 225 229  
FT STRAND 234 234  
FT HELIX 236 244  
FT TURN 245 245  
FT STRAND 246 250  
FT HELIX 252 262  
FT STRAND 263 264  
FT TURN 265 266  
FT STRAND 267 267  
FT HELIX 269 282  
FT STRAND 284 284  
FT HELIX 286 288  
FT STRAND 289 291  
FT STRAND 293 293  
FT TURN 296 297  
FT STRAND 298 298  
FT HELIX 301 303  
FT TURN 304 304  
FT STRAND 321 328  
FT TURN 329 334  
FT TURN 339 343  
FT HELIX 347 350  
FT TURN 351 352  
FT TURN 354 355  
FT HELIX 357 375  
FT TURN 377 381  
FT STRAND 382 382  
FT STRAND 385 390  
FT TURN 391 392  
FT STRAND 393 400  
FT TURN 401 403  
FT STRAND 405 410  
FT STRAND 412 412  
FT TURN 414 415  
FT STRAND 416 416  
FT STRAND 419 423  
FT TURN 430 431  
FT STRAND 432 436  
FT TURN 437 438  
FT STRAND 439 444  
FT TURN 447 448  
FT STRAND 449 449  
FT STRAND 451 455  
FT TURN 457 458  
FT STRAND 461 465  
FT HELIX 466 469  
FT TURN 470 471